* *
Reviewer Comments:

SEQUENCE LISTING

<110>   Hellström, Mats
        Wallgard, Elisabet
        Kalén, Mattias

Please remove the foreign accent marks in the first and third
applicant's names; foreign accent marks are non-ACII characters, which
cannot be processed.

<120>   ANGIOGENESIS-AFFECTING POLYPEPTIDES, PROTEINS, AND COMPOSITIONS,
AND METHODS OF USE THEREOF

The above <120> response exceeds the Sequence Rules' required 72-
character line limit: please adjust the line, by inserting hard
returns.

(from the end of Sequence 52)
Ser Cys Ser Leu Glu Pro Ser Ala Pro Glu Asp Leu Leu
    850   855   860

1

Please remove the "1" above, which appears at the end of the submitted
file.

* *

Application No: 10581761   Version No: 1.0

Input Set:

Output Set:

Started: 2008-04-15 14:49:57.985
Finished: 2008-04-15 14:50:00.843
Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 858 ms
Total Warnings: 30
Total Errors: 2
No. of SeqIDs Defined: 52
Actual SeqID Count: 52

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (1)
W 402	Undefined organism found in <213> in SEQ ID (2)
W 402	Undefined organism found in <213> in SEQ ID (3)
W 402	Undefined organism found in <213> in SEQ ID (6)
W 402	Undefined organism found in <213> in SEQ ID (7)
W 402	Undefined organism found in <213> in SEQ ID (8)
W 402	Undefined organism found in <213> in SEQ ID (11)
W 402	Undefined organism found in <213> in SEQ ID (12)
W 402	Undefined organism found in <213> in SEQ ID (13)
W 402	Undefined organism found in <213> in SEQ ID (16)
W 402	Undefined organism found in <213> in SEQ ID (17)
W 402	Undefined organism found in <213> in SEQ ID (18)
W 402	Undefined organism found in <213> in SEQ ID (23)
W 402	Undefined organism found in <213> in SEQ ID (24)
W 402	Undefined organism found in <213> in SEQ ID (25)
W 402	Undefined organism found in <213> in SEQ ID (28)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (30)
W 402	Undefined organism found in <213> in SEQ ID (33)
W 402	Undefined organism found in <213> in SEQ ID (34)

```
              Input Set:


              Output Set:



              Started:    2008-04-15 14:49:57.985
             Finished:    2008-04-15 14:50:00.843
              Elapsed:    0 hr(s) 0 min(s) 2 sec(s) 858 ms
       Total Warnings:    30
         Total Errors:    2
  No. of SeqIDs Defined:  52
    Actual SeqID Count:   52
```

Error code   Error Description

        `This error has occured more than 20 times, will not be displayed`

E   355   `Empty lines found between the amino acid numbering and the`

E   321   `No. of Bases conflict, this line has no nucleotides  SEQID (52)`

```
<210>  1
<211>  736
<212>  DNA
<213>  Murinae gen. sp.

<400>  1
gtgatccagg atccgaagag gcccggagca ggagcatggc gtcgtcgggg tcggtgcagc      60

agctgcccct ggtgctgctg atgttgctgt tggcgagtgc ggcacgggcc agactctact     120

tccgctcggg ccagacttgc taccatccca ttcgcgggga ccagctggct ctgctggggc     180

gcaggactta tcctcggccg catgagtacc tgtccccagc ggatctcccc aagaattggg     240

actggagaaa tgtgaacggt gtcaactatg ccagcgtcac caggaaccag cacatcccac     300

agtactgtgg ttcctgctgg gcccacggca gcaccagtgc catggcagac cgaatcaaca     360

tcaagaggaa aggtgcatgg ccctccatcc tgctgtccgt acagaatgtc attgactgtg     420

gcaatgctgg ctcttgtgaa gggggcaatg accttccggt gtgggagtat gcccacaagc     480

atggcatccc cgatgagacc tgcaacaact accaggcaag gaccaagact gtgacaagtt     540

taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga attacaccct     600

ctggagagtg ggtgattacg gtccctgtcc gggagggaga agatgatggc gagatctatg     660

ccaatggtcc catcagctgc gggataatgg gcaccagaga tgatgtctaa ctacactggg     720

ggcatctatg ctgagc                                                    736


<210>  2
<211>  1404
<212>  DNA
<213>  Murinae gen. sp.

<400>  2
aaaggaccgg gcggggcgtc ccgagcgcgt gggcctgcgg gtcgggtcaa gaggtcgaag      60

gtgctgcgcg tgatccagga tccgaattgg cccggagcag gagcatggcg tcgtcggggt     120

cggtgcagca gctgcccctg gtgctgctga tgttgctgtt ggcgagtgcg gcacgggcca     180

gactctactt ccgctcgggc cagacttgct accatcccat tcgcggggac cagctggctc     240

tgctggggcg caggacttat cctcggccgc atgagtacct gtccccagcg gatctcccca     300

agaattggga ctggagaaat gtgaacggtg tcaactatgc cagcgtcacc aggaaccagc     360

acatcccaca gtactgtggt tcctgctggg cccacggcag caccagtgcc atggcagacc     420

gaatcaacat caagaggaaa ggtgcatggc cctccatcct gctgtccgta cagaatgtca     480

ttgactgtgg caatgctggc tcttgtgaag ggggcaatga ccttccggtg tgggagtatg     540
```

```
cccacaagca tggcatcccc gatgagacct gcaacaacta ccaggccaag gaccaagact    600

gtgacaagtt taaccagtgt gggacctgca ctgaattcaa agagtgtcac accatccaga    660

attcaccct ctggagagtg ggtgattacg gctccctgtc cgggagggag aagatgatgg    720

ccgagatcta tgccaatggt cccatcagct gcgggataat ggcaacagag atgatgtcta    780

actacactgg gggcatctat gctgagcacc aggaccaggc cgttatcaac cacatcatct    840

ctgtagctgg ctggggtgtc agcaacgatg gcatcgagta ctggattgtc cgaaattcat    900

ggggcgaacc ctggggtgag aaaggctgga tgaggatcgt gaccagcacc tacaagggag    960

gcacaggtga cagctacaac cttgccatcg agagtgcctg cacatttggg accccattg    1020

tttaggtaga tgtctctgga agcagcgctg tgaaccatga caggggaggg tgattaatta    1080

ctgacactgg acatgtccag acagctataa acagtgcttg tggacatgag accagagtg    1140

tggactgcat cccgagagga gacggtaaag gatgaaacac aactgcactg ggaccctccg    1200

ccgtaccctc caggcctgcc tcctccacca ctgagccctc caggcctgcc tcctcttcta    1260

cagtgcttgc cttcagccac ccggagaaga gagctatggt ttaggacagc tcaacttatc    1320

accagatctg gagccctgga atccatggga ggggggaaca agtccagact gcttaagaaa    1380

tgagtaaaat atctggcttc ccac                                          1404


<210>  3
<211>  306
<212>  PRT
<213>  Murinae gen. sp.

<400>  3

Met Ala Ser Ser Gly Ser Val Gln Gln Leu Pro Leu Val Leu Leu Met
1               5                   10                  15


Leu Leu Leu Ala Ser Ala Ala Arg Ala Arg Leu Tyr Phe Arg Ser Gly
                20                  25                  30


Gln Thr Cys Tyr His Pro Ile Arg Gly Asp Gln Leu Ala Leu Leu Gly
            35                  40                  45


Arg Arg Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu
        50                  55                  60


Pro Lys Asn Trp Asp Trp Arg Asn Val Asn Gly Val Asn Tyr Ala Ser
65                  70                  75                  80
```

Val Thr Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala
                    85   90   95

His Gly Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys
            100   105   110

Gly Ala Trp Pro Ser Ile Leu Leu Ser Val Gln Asn Val Ile Asp Cys
            115   120   125

Gly Asn Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Pro Val Trp Glu
        130   135   140

Tyr Ala His Lys His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln
145   150   155   160

Ala Lys Asp Gln Asp Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Thr
            165   170   175

Glu Phe Lys Glu Cys His Thr Ile Gln Asn Tyr Thr Leu Trp Arg Val
            180   185   190

Gly Asp Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile
        195   200   205

Tyr Ala Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Met Met
    210   215   220

Ser Asn Tyr Thr Gly Gly Ile Tyr Ala Glu His Gln Asp Gln Ala Val
225   230   235   240

Ile Asn His Ile Ile Ser Val Ala Gly Trp Gly Val Ser Asn Asp Gly
            245   250   255

Ile Glu Tyr Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu
            260   265   270

Lys Gly Trp Met Arg Ile Val Thr Ser Thr Tyr Lys Gly Gly Thr Gly
        275   280   285

Asp Ser Tyr Asn Leu Ala Ile Glu Ser Ala Cys Thr Phe Gly Asp Pro
        290   295   300

Ile Val
305

<210> 4
<211> 1480
<212> DNA
<213> Homo sapiens

<400> 4
ctgggccgag gccgaggccg gggcgggatc cagagcggga gccggcgcgg gatctgggac   60

tcggagcggg atccggagcg ggacccagga gccggcgcgg ggccatggcg aggcgcgggc   120

cagggtggcg gccgcttctg ctgctcgtgc tgctggcggg cgcggcgcag ggcggcctct   180

acttccgccg gggacagacc tgctaccggc ctctgcgggg ggacgggctg gctccgctgg   240

ggcgcagcac ataccccggg cctcatgagt acctgtcccc agcggatctg cccaagagct   300

gggactggcg caatgtggat ggtgtcaact atgccagcat caccggaac cagcacatcc   360

cccaatactg cggctcctgc tgggcccacg ccagcaccag cgctatggcg gatcggatca   420

acatcaagag gaagggagcg tggccctcca ccctcctgtc cgtgcagaac gtcatcgact   480

gcggtaacgc tggctcctgt gaagggggta atgacctgtc cgtgtgggac tacgcccacc   540

agcacggcat ccctgacgag acctgcaaca ctaccaggc caaggaccag gagtgtgaca   600

agtttaacca atgtgggaca tgcaatgaat tcaaagagtg ccacgccatc cggaactaca   660

ccctctggag ggtgggagac tacggctccc tctctgggag ggagaagatg atggcagaaa   720

tctatgcaaa tggtcccatc agctgtggaa taatggcaac agaaagactg gctaactaca   780

ccggaggcat ctatgccgaa taccaggaca ccacatatat aaaccatgtc gtttctgtgg   840

ctgggtgggg catcagtgat gggactgagt actggattgt ccggaattca tggggtgaac   900

catgggggga gagaggctgg ctgaggatcg tgaccagcac ctataaggat gggaagggcg   960

ccagatacaa ccttgccatc gaggagcact gtacatttgg gaccccatc gtttaaggcc   1020

atgtcactag aagcgcagtt taagaaaagg catggtgacc catgaccaga ggggatccta   1080

tggttatgtg tgccaggctg ctggcagga ctggggtgg ctatcaatat ggatggcga   1140

ggacagcgtg gcactggctg cgagtgttcc tgagagttga aagtgggatg acttatgaca   1200

cttgcacagc atggctctgc ctcacaatga tgcagtcagc cacctggtga agaagtgacc   1260

tgcgacacag gaaacgatgg gacctcagtc ttcttcagca gaggacttga tattttgtat   1320

ttggcaactg tgggcaataa tatggcattt aagaggtgaa agagttcaga cttatcacca   1380

ttcttatgtc actttagaat caagggtggg ggagggaggg agggagttgg cagtttcaaa   1440

tcgcccaagt gatgaataaa gtatctggct ctgcacgaga   1480

<210>   5
<211>   303
<212>   PRT
<213>   Homo sapiens

<400>   5

Met Ala Arg Arg Gly Pro Gly Trp Arg Pro Leu Leu Leu Val Leu
1   5   10   15

Leu Ala Gly Ala Ala Gln Gly Gly Leu Tyr Phe Arg Arg Gly Gln Thr
                20   25   30

Cys Tyr Arg Pro Leu Arg Gly Asp Gly Leu Ala Pro Leu Gly Arg Ser
        35   40   45

Thr Tyr Pro Arg Pro His Glu Tyr Leu Ser Pro Ala Asp Leu Pro Lys
        50   55   60

Ser Trp Asp Trp Arg Asn Val Asp Gly Val Asn Tyr Ala Ser Ile Thr
65   70   75   80

Arg Asn Gln His Ile Pro Gln Tyr Cys Gly Ser Cys Trp Ala His Ala
                85   90   95

Ser Thr Ser Ala Met Ala Asp Arg Ile Asn Ile Lys Arg Lys Gly Ala
                100   105   110

Trp Pro Ser Thr Leu Leu Ser Val Gln Asn Val Ile Asp Cys Gly Asn
        115   120   125

Ala Gly Ser Cys Glu Gly Gly Asn Asp Leu Ser Val Trp Asp Tyr Ala
    130   135   140

His Gln His Gly Ile Pro Asp Glu Thr Cys Asn Asn Tyr Gln Ala Lys
145   150   155   160

Asp Gln Glu Cys Asp Lys Phe Asn Gln Cys Gly Thr Cys Asn Glu Phe
                165   170   175

Lys Glu Cys His Ala Ile Arg Asn Tyr Thr Leu Trp Arg Val Gly Asp
                180   185   190

Tyr Gly Ser Leu Ser Gly Arg Glu Lys Met Met Ala Glu Ile Tyr Ala
        195   200   205

Asn Gly Pro Ile Ser Cys Gly Ile Met Ala Thr Glu Arg Leu Ala Asn
        210   215   220

Tyr Thr Gly Gly Ile Tyr Ala Glu Tyr Gln Asp Thr Thr Tyr Ile Asn
225   230   235   240

His Val Val Ser Val Ala Gly Trp Gly Ile Ser Asp Gly Thr Glu Tyr
                245   250   255

Trp Ile Val Arg Asn Ser Trp Gly Glu Pro Trp Gly Glu Arg Gly Trp
                260   265   270

Leu Arg Ile Val Thr Ser Thr Tyr Lys Asp Gly Lys Gly Ala Arg Tyr
        275   280   285

Asn Leu Ala Ile Glu Glu His Cys Thr Phe Gly Asp Pro Ile Val
        290   295   300

<210>   6
<211>   646
<212>   DNA
<213>   Murinae gen. sp.

<400>   6
tcctttccta gtctgtcttc agatgaaacc tattctctgc ttgtacaaga accagtagcc   60

gtcctcaagg ccaacagcgt tggggagcgt tacgaggttt agagacgttt agccagttag   120

tttaccaaga ctctttcggg actttcacca tcaatgaatc cagtatagct gattctccaa   180

gattccctca tagaggaatt ttaattgata catctagaca cttcctgcct gtgaagacaa   240

ttttaaaaac tctggatgcc atggctttta ataagtttaa tgttcttcac tggcacatag   300

tggacgacca gtctttccct tatcagagta ccacttttcc tgagctaagc aataagggaa   360

gctactcttt gtctcatgtc tatacaccaa acgatgtccg gatggtgctg gagtacgccc   420

ggctccgagg gattcgagtc ataccagaat ttgatacccc tggccataca cagtcttggg   480

gcaaaggaca gaaaaacctt ctaactccat gttacaatca aaaaactaaa actcaagtgt   540

ttgggcctgt agacccaact gtaaacacaa cgtatgcatt ctttaacaca tttttcaaag   600

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aaatcagcag tgtgtttcca gatcagttca tccacttggg aggaga                    646


<210>  7
<211>  1805
<212>  DNA
<213>  Murinae gen. sp.

<400>  7
ggatgctttc ttcccagcga cccagactgg aaggttggtc caaagactgc ctagccagac       60

tcgcggagca gtcatgccgc agtccccgcg tagcgccccc gggctgctgc tgctgcaggc      120

gctggtgtcg ctagtgtcgc tggccctagt ggccccggcc cgactgcaac ctgcgctatg      180

gcccttcccg cgctcggtgc agatgttccc gcggctgttg tacatctccg cggaggactt      240

cagcatcgac cacagtccca attccacagc gggcccttcc tgctcgctgc tacaggaggc      300

gtttcggcga tattacaact atgtttttgg tttctacaag agacatcatg gccctgctag      360

atttcgagct gagccacagt tgcagaagct cctggtctcc attaccctcg agtcagagtg      420

cgagtccttc cctagtctgt cttcagatga aacctattct ctgcttgtac aagaaccagt      480

agccgtcctc aaggccaaca gcgtttgggg agcgttacga ggtttagaga cgtttagcca      540

gttagtttac caagactctt tcgggacttt caccatcaat gaatccagta tagctgattc      600

tccaagattc cctcatagag gaattttaat tgatacatct agacacttcc tgcctgtgaa      660

gacaatttta aaaactctgg atgccatggc ttttaataag tttaatgttc ttcactggca      720

catagtggac gaccagtctt tcccttatca gagtaccact tttcctgagc taagcaataa      780

gggaagctac tctttgtctc atgtctatac accaaacgat gtccggatgg tgctggagta      840

cgcccggctc cgagggattc gagtcatacc agaatttgat acccctggcc atacacagtc      900

ttggggcaaa ggacagaaaa accttctaac tccatgttac aatcaaaaaa ctaaaactca      960

agtgtttggg cctgtagacc caactgtaaa cacaacgtat gcattcttta acacattttt     1020

caaagaaatc agcagtgtgt ttccagatca gttcatccac ttgggaggag atgaagtaga     1080

atttcaatgt tgggcatcaa atccaaacat ccaaggtttc atgaagagaa agggctttgg     1140

cagcgatttt agaagactag aatccttta tattaaaaag attttggaaa ttatttcatc     1200

cttaaagaag aactccattg tttggcaaga agttttgat gataaggtgg agcttcagcc     1260

gggcacagta gtcgaagtgt ggaagagtga gcattattca tatgagctaa agcaagtcac     1320

aggctctggc ttccctgcca tcctttctgc tccttggtac ttagacctga tcagctatgg     1380

gcaagactgg aaaaactact acaaagttga gcccccttaat tttgaaggct ctgagaagca     1440
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gaaacaactt gttattggtg gagaagcttg cctgtgggga gaatttgtgg atgcaactaa    1500

ccttactcca agattatggc ctcgagcaag cgctgttggt gagagactct ggagccctaa    1560

aactgtcact gacctagaaa atgcctacaa acgactggcc gtgcaccgct gcagaatggt    1620

cagccgtgga atagctgcac aacctctcta tactggatac tgtaactatg agaataaaat    1680

atagaagtga cagacgtcta cagcattcca gctatgatca tgttgattct gaaatcatgt    1740

aaattaagat ttgttaggct gttttttttt taaataaacc atcttttat tgattgaatc    1800

tttct                                                              1805


<210>   8
<211>   536
<212>   PRT
<213>   Murinae gen. sp.

<400>   8

Met Pro Gln Ser Pro Arg Ser Ala Pro Gly Leu Leu Leu Gln Ala
1                   5                   10                  15


Leu Val Ser Leu Val Ser Leu Ala Leu Val Ala Pro Ala Arg Leu Gln
            20                  25                  30


Pro Ala Leu Trp Pro Phe Pro Arg Ser Val Gln Met Phe Pro Arg Leu
        35                  40                  45


Leu Tyr Ile Ser Ala Glu Asp Phe Ser Ile Asp His Ser Pro Asn Ser
    50                  55                  60


Thr Ala Gly Pro Ser Cys Ser Leu Leu Gln Glu Ala Phe Arg Arg Tyr
65                  70                  75                  80


Tyr Asn Tyr Val Phe Gly Phe Tyr Lys Arg His His Gly Pro Ala Arg
                85                  90                  95


Phe Arg Ala Glu Pro Gln Leu Gln Lys Leu Leu Val Ser Ile Thr Leu
                100                 105                 110


Glu Ser Glu Cys Glu Ser Phe Pro Ser Leu Ser Ser Asp Glu Thr Tyr
            115                 120                 125


Ser Leu Leu Val Gln Glu Pro Val Ala Val Leu Lys Ala Asn Ser Val
    130                 135                 140
```

Trp Gly Ala Leu Arg Gly Leu Glu Thr Phe Ser Gln Leu Val Tyr Gln
145   150   155   160

Asp Ser Phe Gly Thr Phe Thr Ile Asn Glu Ser Ser Ile Ala Asp Ser
                165   170   175

Pro Arg Phe Pro His Arg Gly Ile Leu Ile Asp Thr Ser Arg His Phe
                180   185   190

Leu Pro Val Lys Thr Ile Leu Lys Thr Leu Asp Ala Met Ala Phe Asn
            195   200   205

Lys Phe Asn Val Leu His Trp His Ile Val Asp Asp Gln Ser Phe Pro
            210   215   220

Tyr Gln Ser Thr Thr Phe Pro Glu Leu Ser Asn Lys Gly Ser Tyr Ser
225   230   235   240

Leu Ser His Val Tyr Thr Pro Asn Asp Val Arg Met Val Leu Glu Tyr
                245   250   255

Ala Arg Leu Arg Gly Ile Arg Val Ile Pro Glu Phe Asp Thr Pro Gly
            260   265   270

His Thr Gln Ser Trp Gly Lys Gly Gln Lys Asn Leu Leu Thr Pro Cys
            275   280   285

Tyr Asn Gln Lys Thr Lys Thr Gln Val Phe Gly Pro Val Asp Pro Thr
            290   295   300

Val Asn Thr Thr Tyr Ala Phe Phe Asn Thr Phe Phe Lys Glu Ile Ser
305   310   315   320

Ser Val Phe Pro Asp Gln Phe Ile His Leu Gly Gly Asp Glu Val Glu
                325   330   335

Phe Gln Cys Trp Ala Ser Asn Pro Asn Ile Gln Gly Phe Met Lys Arg
                340   345   350

Lys Gly Phe Gly Ser Asp Phe Arg Arg Leu Glu Ser Phe Tyr Ile Lys
            355   360   365

Lys Ile Leu Glu Ile Ile Ser Ser Leu Lys Lys Asn Ser Ile Val Trp
    370   375   380

Gln Glu Val Phe Asp Asp Lys Val Glu Leu Gln Pro Gly Thr Val Val
385   390   395   400

Glu Val Trp Lys Ser Glu His Tyr Ser Tyr Glu Leu Lys Gln Val Thr
                405   410   415

Gly Ser Gly Phe Pro Ala Ile Leu Ser Ala Pro Trp Tyr Leu Asp Leu
                420   425   430

Ile Ser Tyr Gly Gln Asp Trp Lys Asn Tyr Tyr Lys Val Glu Pro Leu